



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/053,530

DATE: 02/13/2002  
TIME: 09:53:15

Input Set : A:\401.app.txt  
Output Set: N:\CRF3\02132002\J053530.raw

Does Not Comply  
Corrected Diskette Needed

P3

3 <110> APPLICANT: Ledbetter, Jeffrey  
4 Hayden-Ledbetter, Martha  
6 <120> TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins  
8 <130> FILE REFERENCE: 390069.401  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/053,530  
13 <141> CURRENT FILING DATE: 2002-01-17  
15 <150> PRIOR APPLICATION NUMBER: US 09/765,208  
16 <151> PRIOR FILING DATE: 2001-01-17  
18 <160> NUMBER OF SEQ ID NOS: 38  
20 <170> SOFTWARE: PatentIn version 3.0  
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38 <223> OTHER INFORMATION: light chain variable region for anti-CD20 scFv  
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56 ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgttaaggta catgcactgg 180  
57 taccaggcaga agccagggatc ctccccccaaa ccctggattt atgccccatc caaccctggct 240  
58 tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
59 agcagagtgg aggtcagaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360  
60 cccacgttcg gtgctggac caagctggag ctgaaagggtt gccggggctc gggcggttgt 420  
61 ggtatctggag gaggtggag ctctcaggct tatctacagc agtctggggc tgagctggtg 480  
62 aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gtcacacatt taccagttac 540  
63 aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
64 ccagggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660

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 101 <223> OTHER INFORMATION: HUMAN IgG1 Fc TAIL, WILD TYPE HINGE, CH2 AND CH3  
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 109 ccaggggaga aggtcacaat gacttgcagg gccagctaa gtgttaaggta catgcactgg 180  
 111 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
 113 tctggagttcc ctgctcgctt cagttggcgtt gggcttggga cctcttactc tetcacaatc 300  
 115 agcagagtgg aggctgaaga tgctgcccact tattactgcc agcagtggag ttttaaccca 360  
 117 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgg 420  
 119 ggatctggag gaggtgggag ctctcaggtt tatctacagc agtctggggc tgagctgg 480  
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 123 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttt 600  
 125 ccagggaaatg gtgatacttc ctacaatcag aagtcaagg gcaaggccac actgactgta 660  
 127 gacaaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg 720  
 129 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtaactt cgatgtctgg 780  
 131 ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttgtga caaaactcac 840  
 133 acatgcccac cgtgcccagc acctgaactc ctgggggac cgtcagtctt cctttcccc 900  
 135 caaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtgggtgg 960  
 137 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020  
 139 cataatgccca agacaaagcc gcggggaggag cagttacaaca gcacgtaccc tgggtcagc 1080  
 141 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140  
 143 aacaaaagccc tcccagcccc catcgagaaa acaatctcca aagccaaagg gcagccccga 1200  
 145 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260  
 147 ctgacctgcc tggtaaaagg cttctatccc agcgacatcg cctggagtg ggagagcaat 1320  
 149 gggcagccgg agaacaacta caagaccacg ctcacgtgc tggactccga cggctccctc 1380  
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 160 <212> TYPE: DNA  
 161 <213> ORGANISM: Artificial Sequence  
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 175 <223> OTHER INFORMATION: HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES  
 176 PROLINE TO SERINE MUTATION (880-883) IN CH2 DISRUPTS EFFECTOR FUN  
 177 CTION  
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 183 gtcataattt ccagaggaca aattgttctc tccca gtc cagcaat cct gtctgc at ct 120  
 185 ccaggggaga aggtcacaat gacttgcagg gccagctaa gtgtaa gttt catgcactgg 180  
 187 taccagcaga agccaggatc ctcccccaaa ccctggattt at gccc atc caacctggct 240  
 189 tctggagttc ctgc tgc ctt cagtggc agt ggtt ctggga ccttta actc ttc tacaatc 300  
 191 agcagagttg aggctgaaga tgctgc cact tattactgc agc agtggag tttt aaccca 360  
 193 cccacgttgc gtgc tgggac caagctggag ctgaa aagatg ggc ggtt gctc gggcggtgg 420  
 195 ggc atctggag gaggtgggag ctctc aggtt cttt tatctacgc agtctgggatc tgagctgg 480  
 197 aggcctgggg cctc agt gaa gatgtc tgc aaggcttctg gctacacatt taccaggat 540  
 199 aatatgcact gggtaa agca gacac ctaga caggcctgg aatggatgg agtattttat 600  
 201 ccaggaaatg gtgata cttc tca aatc ag aagtcaagg gcaaggccac actgactgt 660  
 203 gacaaatcct ccagcacagc tca atgc agt ctc agc tgacatctg agactctgc 720  
 205 gtctatttct gtgcaagatg ggtt tactat agt aactctt actgg tactt cgtatgtctgg 780  
 207 ggcacagggc ccacgg tca cgtt ctgtat caggagccca aatcttctg caaaaactcac 840  
 209 acatccccac cgtccccagc acctgaa actc ctgggggat cgtc agt ct tttt ccttcccc 900  
 211 ccaaaaccca aggacacccct catgatctt cggacccctg aggtc acatg cgtgg tgg 960  
 213 gacgtgagcc acga aagaccc ttgagg tcaag ttca actt ggtt acgtgg acgg cgtgg ggg 1020  
 215 cataatgcacca agaca aagcc gggggaggag cag taca aaca gcacgt accg tgg tca 1080  
 217 gtcctc accgg tcctgc ac ca ggactggctg aatggcaagg agtaca agt gcaagg tctcc 1140  
 219 aaca aagcc tccca gccc catc gagaaa acaatctca aagccaaagg gca gccc gaa 1200  
 221 gaaccacagg tgc tacc cctt gccc catcc cggatg agc tgacca agaa ccagg tca 1260  
 223 ctgacctg cttt ggtt caaagg ct tctatccc agc gac atc g cgtgg agt ggag agcaat 1320  
 225 gggc aga aacacta caa gaccc acg cttcc cgtgc tggactccga cggcccttc 1380  
 227 ttcctctaca gca agt ctc ac cgtgg aca agc aggtt ggc agc aagg gaa cgtt ctca 1440  
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251 <222> LOCATION: (808)..(1513)  
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253 WILD TYPE CH2 AND CH3 DOMAINS MEDIATE EFFECTOR FUNCTIONS  
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261 ccaggggaga	aggtcacaat	gacttgcagg	gccagctaa	gtgtaa	ggtt	catgc	actgg	180
263 taccagcaga	agccaggatc	ctccccccaa	ccctggattt	atgccc	atc	caac	ctggct	240
265 tctggagtcc	ctgctcgctt	cagtggcagt	gggtctggga	cctt	taactc	tctc	cacaatc	300
267 agcagagtg	aggctgaaga	tgctgccact	tattactg	cc	agcagtgg	ggag	tttt	360
269 cccacgttcg	gtgctgggac	caagctggag	ctgaaa	agatg	gcgg	ttgg	ctc	420
271 ggatctggag	gaggtgggag	ctctcag	ggtt	tat	tctgg	ggc	tgag	480
273 aggcttg	ggg	cctcag	gtgt	cc	tctgc	aagg	ttctg	540
275 aatatgcact	gggttaaagca	gacac	ctt	gac	atc	tttt	tttt	600
277 ccaggaaatg	gtgata	acttc	ctaca	atc	agtt	caagg	gcaagg	660
279 gacaaatc	ccag	cac	atc	atc	tgac	atc	tttgc	720
281 gtctattt	gt	caag	atg	gtt	tactat	atg	tttgc	780
283 ggcacagg	ga	cac	gg	tcac	ctgt	ttt	atgt	840
285 acatccccac	cg	tccc	cc	tcac	actc	ttt	tcac	900
287 ccaaaaccca	agg	accc	ct	catg	atcc	cc	atc	960
289 gacgtgag	cc	ac	aa	gac	tttgc	ttt	atgt	1020
291 cataatgcca	ag	aca	aa	agcc	tttgc	ttt	atgt	1080
293 gtcctcac	cc	tcc	tc	atc	tttgc	ttt	atgt	1140
295 aacaaagccc	tcc	cag	ccc	catc	atcc	cc	atc	1200
297 gaaccacagg	tgt	ac	cc	atcc	tttgc	ttt	atgt	1260
299 ctgac	ct	gt	cc	atcc	tttgc	ttt	atgt	1320
301 gggcagccg	aga	aca	acta	caag	atcc	cc	atc	1380
303 ttcctctaca	gca	agc	tac	tc	tttgc	ttt	atgt	1440
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342	gtcacaatga cttgcaggc cagctcaagt gtaaattaca	tgcactgta ccagcagaag	180
344	ccaggatctt ccccaaaacc ctggatttat gccccatcca	acctggcttc tggagtccct	240
346	gctcgcttca gtggcagtgg gtctgggacc tcttactctc	tcacaatcag cagagtggag	300
348	gctgaagatg ctgcactta ttactgccag cagtggagtt	ttaaccacc cacgttcgg	360
350	gctgggacca agctggagct gaaagatggc ggtggctgg	gcccgtggg atctggagga	420
352	ggtgggagct ctcaggctt tctacagcag tctgggctg	agctggtag ggcctgggccc	480
354	tcagtgaaga tgtcctgcaa ggcttctggc tacacattta	ccagttacaa tatgcactgg	540
356	gtaaaggcaga cacctagaca gggcctggaa tggattggag	ctatttatcc agggaaatgg	600
358	gataacttctc acaatcagaa gttcaaggc aaggccacac	tgactgtaga caaatccctc	660
360	agcacagcct acatgcagct cagcagctg acatctgaag	actctgcggg ctatttctgt	720
362	gcaagagttgg tgtactatag taactcttac tggtaacttcg	atgtctggg cacagggacc	780
364	acggtcaccc tctctgtatca gccagttccc tcaactccac	ctacccatc tccctcaact	840
366	ccacccatcc catctccctc atgcgcaccc	gaactctgg ggggaccggtc agtcttcctc	900
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370	gtgggtggacg tgagccacga agacccttagt	gtcaagttca actggtagt ggacggcg	1020
372	gaggtgcata atgccaagac aaagccgcgg	gaggagcgt acaacagcac gtaccgtgt	1080
374	gtcagcgtcc tcaccgtctc gcaccaggac	tggctgaatg gcaaggagta caagtcaag	1140
376	gtctccaaaca aaggccctccc agcccccattc	gagaaaacaa tctccaaacg caaaggccag	1200
378	ccccgagaac cacaggtgtc caccctgtcc	ccatcccggt atgagctgac caagaaccag	1260
380	gtcagcgtca cctgccttgc	caaaggcttc tatcccagcg acatgcgtt ggagtggag	1320
382	agcaatgggc agccggagaa caactacaag accacgcctc	ccgtctgggatccgc	1380
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411	tcccgaccc ctgaggtcac atgcgtggg	gtggacgtga gccacgaaga ccctgagg	180
413	aagtcaact ggtacgtggc cggcgtggag	gtgcataatg ccaagacaaa gccgcgggag	240
415	gagcagtaca acagcacgtc ccgtgtggc	agcgtctca ccgtctgtca ccaggactgg	300
417	ctgaatggca aggatcacaa gtgcaggc	tccaaacaaag ccctcccgac cccatcgag	360
419	aaaacaatct ccaaagccaa agggcagccc	cgagaaccac aggtgtacac cctgc	420
421	tcccgatggat agctgaccaa gaaccaggc	agcgtaccccttgc	480
423	cccaaggcaca tcgcccgtgg	gtgggagagc aatgggcagc cggagaacaa	540
425	acgcctcccg tgctggactc	cgacggctcc ttcttcttcc acagcaagct caccgtggac	600
427	aagagcagggt ggcagcagg	gaacgtcttc tcatgtcccg tgatgtatgc	660
429	aaccactaca cgcagaagag	ccttcgggtaaatgtatctag a	711

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